

AMENDMENTS TO THE CLAIMS

Listing of Claims:

1. (Currently amended) A process for preparing ketocarotenoids by cultivating genetically modified organisms which, compared with the wild type, have a modified ketolase activity, and the modified ketolase activity is caused by a ketolase comprising the amino acid sequence SEQ ID NO: 2 or a sequence which is derived from this sequence by substitution, insertion or deletion of amino acids and which has an identity of at least 42% 95% at the amino acid level with the sequence SEQ ID NO: 2.
2. (Previously presented) The process as claimed in claim 1, wherein organisms which, as wild type, already have a ketolase activity, and the genetic modification brings about an increase in the ketolase activity compared with the wild type, are used.
3. (Currently amended) The process as claimed in claim 1, wherein the ketolase activity is increased by increasing the gene expression of a nucleic acid encoding a ketolase comprising the amino acid sequence SEQ ID NO: 2 or a sequence which is derived from this sequence by substitution, insertion or deletion of amino acids and which has an identity of at least 42% 95% at the amino acid level with the sequence SEQ ID NO: 2, compared with the wild type.
4. (Currently amended) The process as claimed in claim 3, wherein the gene expression is increased by introducing nucleic acids which encode ketolases comprising the amino acid sequence SEQ ID NO: 2 or a sequence which is derived from this sequence by substitution, insertion or deletion of amino acids and which has an identity of at least 42% 95% at the amino acid level with the sequence SEQ ID NO: 2, compared with the wild type, into the organism.
5. (Previously presented) The process as claimed in claim 1, wherein organisms which, as wild type, have no ketolase activity are used, and the genetic modification causes a ketolase activity compared with the wild type.
6. (Currently amended) The process as claimed in claim 5, wherein genetically modified

organisms which transgenically express a ketolase comprising the amino acid sequence SEQ ID NO: 2 or a sequence which is derived from this sequence by substitution, insertion or deletion of amino acids and which has an identity of at least 42% 95% at the amino acid level with the sequence SEQ ID NO: 2, are used.

7. (Currently amended) The process as claimed in claim 5, wherein the gene expression is caused by introducing nucleic acids which encode ketolases comprising the amino acid sequence SEQ ID NO: 2 or a sequence which is derived from this sequence by substitution, insertion or deletion of amino acids and which has an identity of at least 42% 95% at the amino acid level with the sequence SEQ ID NO: 2, into the organism.

8. (Previously presented) The process as claimed in claim 5, wherein nucleic acids comprising the sequence SEQ ID NO: 1 are introduced.

9. (Previously presented) The process as claimed in claim 1, wherein the organisms additionally have an increased activity, compared with the wild type, of at least one of the activities selected from the group of hydroxylase activity and β -cyclase activity.

10. (Previously presented) The process as claimed in claim 9, wherein the gene expression of at least one nucleic acid selected from the group of nucleic acids encoding a hydroxylase, and nucleic acids encoding a β -cyclase, is increased compared with the wild type for the additional increase in at least one of the activities.

11. (Previously presented) The process as claimed in claim 10, wherein the gene expression is increased by introducing at least one nucleic acid selected from the group of nucleic acids encoding a hydroxylase and nucleic acids encoding a β -cyclase into the organism.

12. (Currently amended) The process as claimed in claim 11, wherein nucleic acids which encode a hydroxylase comprising the amino acid sequence SEQ ID NO: 16 or a sequence which is derived from this sequence by substitution, insertion or deletion of amino acids and which has

an identity of at least 20% 95% at the amino acid level with the sequence SEQ ID NO: 16 are introduced as nucleic acid encoding a hydroxylase.

13. (Previously presented) The process as claimed in claim 12, wherein nucleic acids comprising the sequence SEQ ID NO: 15 are introduced.

14. (Currently amended) The process as claimed in claim 11, wherein nucleic acids which encode a β -cyclase comprising the amino acid sequence SEQ ID NO: 18 or a sequence which is derived from this sequence by substitution, insertion or deletion of amino acids and which has an identity of at least 20% 95% at the amino acid level with the sequence SEQ ID NO: 18 are introduced as nucleic acid encoding a β -cyclase.

15. (Previously presented) The process as claimed in claim 14, wherein nucleic acids comprising the sequence SEQ ID NO: 17 are introduced.

16. (Previously presented) The process as claimed in claim 1, wherein the genetically modified organisms are harvested after cultivation, and subsequently the ketocarotenoids are isolated from the organisms.

17. (Previously presented) The process as claimed in claim 1, wherein an organism which is able as starting organism naturally or through genetic complementation or reregulation of metabolic pathways to produce carotenoids is used as organism.

18. (Withdrawn) The process as claimed in claim 1, wherein microorganisms or plants are used as organisms.

19. (Withdrawn) The process as claimed in claim 18, wherein bacteria, yeasts, algae or fungi are used as microorganisms.

20. (Withdrawn) The process as claimed in claim 19, wherein the microorganisms are

selected from the group of *Escherichia*, *Erwinia*, *Agrobacterium*, *Flavobacterium*, *Alcaligenes*, *Paracoccus*, *Nostoc*, cyanobacteria of the genus *Synechocystis*, *Candida*, *Saccharomyces*, *Hansenula*, *Phaffia*, *Pichia*, *Aspergillus*, *Trichoderma*, *Ashbya*, *Neurospora*, *Blakeslea*, *Phycomyces*, *Fusarium*, *Haematococcus*, *Phaedactylum tricornatum*, *Volvox* or *Dunaliella*.

21. (Currently amended) The process as claimed in claim 48 J, wherein plants are used as organism.

22. (Previously presented) The process as claimed in claim 21, wherein a plant selected from the families Ranunculaceae, Berberidaceae, Papaveraceae, Cannabaceae, Rosaceae, Fabaceae, Linaceae, Vitaceae, Brassiceae, Cucurbitaceae, Primulaceae, Caryophyllaceae, Amaranthaceae, Gentianaceae, Geraniaceae, Caprifoliaceae, Oleaceae, Tropaeolaceae, Solanaceae, Scrophulariaceae, Asteraceae, Liliaceae, Amaryllidaceae, Poaceae, Orchidaceae, Malvaceae, Illiaceae or Lamiaceae is used as plant.

23. (Previously presented) The process as claimed in claim 22, wherein a plant selected from the plant genera Marigold, *Tagetes erecta*, *Tagetes patula*, *Acacia*, *Aconitum*, *Adonis*, *Arnica*, *Aquilegia*, *Aster*, *Astragalus*, *Bignonia*, *Calendula*, *Caltha*, *Campanula*, *Canna*, *Centaurea*, *Cheiranthus*, *Chrysanthemum*, *Citrus*, *Crepis*, *Crocus*, *Curcubita*, *Cytisus*, *Delonia*, *Delphinium*, *Dianthus*, *Dimorphotheca*, *Doronicum*, *Eschscholtzia*, *Forsythia*, *Fremontia*, *Gazania*, *Gelsemium*, *Genista*, *Gentiana*, *Geranium*, *Gerbera*, *Geum*, *Grevillea*, *Helenium*, *Helianthus*, *Hepatica*, *Heracleum*, *Hibiscus*, *Heliopsis*, *Hypericum*, *Hypochoeris*, *Impatiens*, *Iris*, *Jacaranda*, *Kerria*, *Laburnum*, *Lathyrus*, *Leontodon*, *Lilium*, *Linum*, *Lotus*, *Lycopersicon*, *Lysimachia*, *Marattia*, *Medicago*, *Mimulus*, *Narcissus*, *Oenothera*, *Osmanthus*, *Petunia*, *Photinia*, *Physalis*, *Phytolacca*, *Potentilla*, *Pyracantha*, *Ranunculus*, *Rhododendron*, *Rosa*, *Rudbeckia*, *Senecio*, *Silene*, *Silphium*, *Sinapsis*, *Sorbus*, *Spartium*, *Tecoma*, *Torenia*, *Tragopogon*, *Trollius*, *Tropaeolum*, *Tulipa*, *Tussilago*, *Ulex*, *Viola* or *Zinnia* is used as plant.

24. (Previously presented) The process as claimed in claim 1, wherein the ketocarotenoids are selected from the group of astaxanthin, canthaxanthin, echinenone, 3-hydroxyechinenone,

3'-hydroxyechinenone, adonirubin and adonixanthin.

25. (Currently amended) A genetically modified organism where the genetic modification
- (a) in the case where the wild-type organism already has a ketolase activity, increases the activity of a ketolase compared with the wild type and
 - (b) in the case where the wild-type organism has no ketolase activity, causes the activity of a ketolase compared with the wild type,

and the ketolase activity which has been increased as in (a) or caused as in (b) is caused by a ketolase comprising the amino acid sequence SEQ ID NO: 2 or a sequence which is derived from this sequence by substitution, insertion or deletion of amino acids and which has an identity of at least 42% 95% at the amino acid level with the sequence SEQ ID NO: 2.

26. (Currently amended) The genetically modified organism as claimed in claim 25, wherein ~~the increasing or causing of the ketolase activity is brought about by an increasing or causing of~~ the gene expression of a nucleic acid encoding a ketolase comprising the amino acid sequence SEQ ID NO: 2 or a sequence which is derived from this sequence by substitution, insertion or deletion of amino acids and which has an identity of at least 42% 95% at the amino acid level with the sequence SEQ ID NO: 2, compared with the wild type.

27. (Currently amended) The genetically modified organism as claimed in claim 26, wherein to increase or cause the gene expression nucleic acids which encode ketolases comprising the amino acid sequence SEQ ID NO: 2 or a sequence which is derived from this sequence by substitution, insertion or deletion of amino acids and which has an identity of at least 42% 95% at the amino acid level with the sequence SEQ ID NO: 2, are introduced into the organism.

28. (Currently amended) A genetically modified organism comprising at least one transgenic nucleic acid encoding a ketolase comprising the amino acid sequence SEQ ID NO: 2 or a sequence which is derived from this sequence by substitution, insertion or deletion of amino acids and which has an identity of at least 42% 95% at the amino acid level with the sequence SEQ ID NO: 2.

29. (Currently amended) A genetically modified organism comprising at least two endogenous nucleic acids encoding a ketolase comprising the amino acid sequence SEQ ID NO: 2 or a sequence which is derived from this sequence by substitution, insertion or deletion of amino acids and which has an identity of at least 42% 95% at the amino acid level with the sequence SEQ ID NO: 2.
30. (Previously presented) The genetically modified organism as claimed in claim 25, wherein the genetic modification additionally increases at least one of the activities selected from the group of hydroxylase activity and β -cyclase activity, compared with the wild type.
31. (Previously presented) The genetically modified organism as claimed in claim 25, which is able as starting organism naturally or through genetic complementation to produce carotenoids.
32. (Currently amended) The genetically modified organism as claimed in claim 25, ~~selected from the group of microorganisms or~~ wherein the organism is a plant[[s]].
33. (Withdrawn) The genetically modified organism as claimed in claim 32, wherein the microorganisms are selected from the group of bacteria, yeasts, algae or fungi.
34. (Withdrawn) The genetically modified microorganism as claimed in claim 33, wherein the microorganisms are selected from the group of *Escherichia*, *Erwinia*, *Agrobacterium*, *Flavobacterium*, *Alcaligenes*, *Paracoccus*, *Nostoc*, cyanobacteria of the genus *Synechocystis*, *Candida*, *Saccharomyces*, *Hansenula*, *Pichia*, *Aspergillus*, *Trichoderma*, *Ashbya*, *Neurospora*, *Blakeslea*, *Phycomyces*, *Fusarium*, *Haematococcus*, *Phaedactylum tricornatum*, *Volvax* or *Dunaliella*.
35. (Previously presented) The genetically modified plant as claimed in claim 32, wherein the plants are selected from the families Ranunculaceae, Berberidaceae, Papaveraceae,

Cannabaceae, Rosaceae, Fabaceae, Linaceae, Vitaceae, Brassicaceae, Cucurbitaceae, Primulaceae, Caryophyllaceae, Amaranthaceae, Gentianaceae, Geraniaceae, Caprifoliaceae, Oleaceae, Tropaeolaceae, Solanaceae, Scrophulariaceae, Asteraceae, Liliaceae, Amaryllidaceae, Poaceae, Orchidaceae, Malvaceae, Iliiaceae or Lamiaceae.

36. (Previously presented) The genetically modified plant as claimed in claim 35, wherein the plants are selected from the plant genera Marigold, *Tagetes erecta*, *Tagetes patula*, *Acacia*, *Aconitum*, *Adonis*, *Arnica*, *Aquilegia*, *Aster*, *Astragalus*, *Bignonia*, *Calendula*, *Caltha*, *Campanula*, *Canna*, *Centaurea*, *Cheiranthus*, *Chrysanthemum*, *Citrus*, *Crepis*, *Crocus*, *Curcubita*, *Cytisus*, *Delonia*, *Delphinium*, *Dianthus*, *Dimorphotheca*, *Doronicum*, *Eschscholtzia*, *Forsythia*, *Fremontia*, *Gazania*, *Gelsemium*, *Genista*, *Gentiana*, *Geranium*, *Gerbera*, *Geum*, *Grevillea*, *Helenium*, *Helianthus*, *Hepatica*, *Heracleum*, *Hibiscus*, *Heliopsis*, *Hypericum*, *Hypochocris*, *Impatiens*, *Iris*, *Jacaranda*, *Kerria*, *Laburnum*, *Lathyrus*, *Leontodon*, *Lilium*, *Linum*, *Lotus*, *Lycopersicon*, *Lysimachia*, *Maratia*, *Medicago*, *Mimulus*, *Narcissus*, *Oenothera*, *Osmanthus*, *Petunia*, *Photinia*, *Physalis*, *Phyteuma*, *Potentilla*, *Pyracantha*, *Ranunculus*, *Rhododendron*, *Rosa*, *Rudbeckia*, *Senecio*, *Silene*, *Silphium*, *Sinapsis*, *Sorbus*, *Spartium*, *Tecoma*, *Torenia*, *Tragopogon*, *Trollius*, *Tropaeolum*, *Tulipa*, *Tussilago*, *Ulex*, *Viola* or *Zinnia*.

37. (Previously presented) The genetically modified organisms as claimed in claim 25, where the organism is used as animal or human food.

38. (Previously presented) The genetically modified organisms as claimed in claim 25, where the organism produces ketocarotenoid-containing extracts or animal and human food supplements.

39. (Withdrawn) A ketolase comprising the amino acid sequence SEQ ID NO: 8 or a sequence which is derived from this sequence by substitution, insertion or deletion of amino acids and which has an identity of at least 70% at the amino acid level with the sequence SEQ ID NO: 8, with the proviso that the amino acid sequence SEQ ID NO: 4 is not present.

40. (Withdrawn) A ketolase comprising the amino acid sequence SEQ ID NO: 6 or a sequence which is derived from this sequence by substitution, insertion or deletion of amino acids and which has an identity of at least 70% at the amino acid level with the sequence SEQ ID NO: 6.

41. (Withdrawn) A ketolase comprising the amino acid sequence SEQ ID NO: 12 or a sequence which is derived from this sequence by substitution, insertion or deletion of amino acids and which has an identity of at least 70% at the amino acid level with the sequence SEQ ID NO: 12, with the proviso that the amino acid sequence SEQ ID NO: 6 is not present.

42. (Withdrawn) A ketolase comprising the amino acid sequence SEQ ID NO: 49 or a sequence which is derived from this sequence by substitution, insertion or deletion of amino acids and which has an identity of at least 50% at the amino acid level with the sequence SEQ ID NO: 49, with the proviso that the amino acid sequence SEQ ID NO: 47 is not present.

43. (Withdrawn) A nucleic acid encoding a protein as claimed in claim 39, with the proviso that the sequence SEQ ID NO: 5 is not present.

44. (Withdrawn) A protein comprising the amino acid sequence SEQ ID NO: 4 or a sequence which is derived from this sequence by substitution, insertion or deletion of amino acids and which has an identity of at least 70% at the amino acid level with the sequence SEQ ID NO: 4, and which has the property of a ketolase.

45. (Withdrawn) A protein comprising the amino acid sequence SEQ ID NO: 6 or a sequence which is derived from this sequence by substitution, insertion or deletion of amino acids and which has an identity of at least 65% at the amino acid level with the sequence SEQ ID NO: 6, and which has the property of a ketolase.

46. (Withdrawn) A protein comprising the amino acid sequence SEQ ID NO: 47 or a sequence which is derived from this sequence by substitution, insertion or deletion of amino

acids and which has an identity of at least 50% at the amino acid level with the sequence SEQ ID NO: 47 and which has the property of a ketolase.

47. (Previously presented) The process as claimed in claim 22, wherein the plant is a plant from the family Asteraceae.

48. (Currently amended) The process as claimed in claim 23, wherein the plant is Tagetes erecta.

49. (Previously presented) The process as claimed in claim 3, wherein the nucleic acid encoding a ketolase comprises the amino acid sequence of SEQ ID NO: 2.

50. (Previously presented) The process as claimed in claim 4, wherein the nucleic acids which encode ketolases comprise the amino acid sequence of SEQ ID NO: 2.

51. (Previously presented) The process as claimed in claim 12, wherein the nucleic acids which encode a hydroxylase comprise the amino acid sequence SEQ ID NO: 16.

52. (Previously presented) The process as claimed in claim 14, wherein the nucleic acids which encode a β -cyclase comprise the amino acid sequence SEQ ID NO: 18.